

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
6260	0.049016	catenin (cadherin-associated protein), beta 1, 88kDa (CTNNA1), mRNA /cds=(215,2560) /gb=NM_001904 /gi=4503130 /ug=Hs.171271 /len=3362	NM_001904	Hs.171271
4129	0.049016	UI-H-DT0-aue-f-11-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5868298 3', mRNA sequence /clone=IMAGE:5868298 /clone_end=3' /gb=BQ030407 /gi=19765686 /ug=Hs.374637 /len=991	BQ030407	Hs.374637
6693	0.049016	PHD finger protein 1 (PHF1), transcript variant 2, mRNA /cds=(216,1919) /gb=NM_024165 /gi=13435396 /ug=Hs.166204 /len=2260	NM_024165	Hs.166204
8586	0.049016	UPF3 regulator of nonsense transcripts A (yeast) (UPF3A), transcript variant 1, mRNA /cds=(38,1468) /gb=NM_023011 /gi=18375523 /ug=Hs.399740 /len=2381	NM_023011	Hs.399740
3736	0.049016	K-ras oncogene protein mRNA, complete cds	M54968	Hs.433714
3962	0.049016	estrogen receptor binding site associated, antigen, 9 (EBAG9), mRNA /cds=(362,1003) /gb=NM_004215 /gi=14577926 /ug=Hs.9222 /len=1182	NM_004215	Hs.9222
14042	0.049016	UI-H-DT0-atw-d-24-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5865191 3', mRNA sequence /clone=IMAGE:5865191 /clone_end=3' /gb=BM994000 /gi=19718901 /ug=Hs.395775 /len=1181	BM994000	Hs.395775
6558	0.049016	ribosomal protein S23 (RPS23), mRNA /cds=(32,463) /gb=NM_001025 /gi=14790142 /ug=Hs.3463 /len=506	NM_001025	Hs.3463
1583	0.049016	BTB (POZ) domain containing 1 (BTBD1), mRNA /cds=(84,1532) /gb=NM_025238 /gi=13376847 /ug=Hs.21332 /len=3177	NM_025238	Hs.21332
2208	0.049016	ribosomal protein S15a (RPS15A), mRNA /cds=(84,476) /gb=NM_001019 /gi=14165468 /ug=Hs.433406 /len=541	NM_001019	Hs.433406
13747	0.049016	hypothetical protein MGC23401 (MGC23401), mRNA /cds=(258,1334) /gb=NM_144982 /gi=21450672 /ug=Hs.245383 /len=1510	NM_144982	Hs.245383
1561	0.049016	translocating chain-associating membrane protein (TRAM), mRNA /cds=(92,1216) /gb=NM_014294 /gi=19923404 /ug=Hs.4147 /len=2722	NM_014294	Hs.4147
6874	0.049016	DNA fragmentation factor, 45kDa, alpha polypeptide (DFFA), mRNA /cds=(57,1052) /gb=NM_004401 /gi=4758147 /ug=Hs.105658 /len=1633	NM_004401	Hs.105658
5506	0.049016	xf26f10.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2619211 3', mRNA sequence /clone=IMAGE:2619211 /clone_end=3' /gb=AW130007 /gi=6131612 /ug=Hs.389726 /len=423	AW130007	Hs.389726
2883	0.049016	thymosin, beta 10 (TMSB10), mRNA /cds=(66,200) /gb=NM_021103 /gi=10863894 /ug=Hs.76293 /len=453	NM_021103	Hs.76293

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4478	0.049016	arginase, type II (ARG2), nuclear gene encoding mitochondrial protein, mRNA /cds=(39,1103) /gb=NM_001172 /gi=10947110 /ug=Hs.172851 /len=1886	NM_001172	Hs.172851
4212	0.049016	chromosome 14 open reading frame 100 (C14orf100), mRNA /cds=(87,1022) /gb=NM_016475 /gi=21361536 /ug=Hs.170219 /len=1692	NM_016475	Hs.170219
13134	0.049016	sine oculis homeobox 2 (Drosophila) (SIX2), mRNA /cds=(283,1158) /gb=NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141	NM_016932	Hs.101937
2814	0.049016	similar to rat tricarboxylate carrier-like protein (BA108L7.2), mRNA /cds=(75,1040) /gb=NM_030971 /gi=13569945 /ug=Hs.283844 /len=2735	NM_030971	Hs.283844
12754	0.049016	ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(38,430) /gb=NM_033022 /gi=14916500 /ug=Hs.180450 /len=537	NM_033022	Hs.180450
13453	0.04655	mesoderm induction early response 1 (MI-ER1), mRNA /cds=(234,1844) /gb=NM_020948 /gi=24308260 /ug=Hs.222746 /len=4972	NM_020948	Hs.222746
13151	0.04655	cell division cycle associated 4 (CDCA4), transcript variant 1, mRNA /cds=(164,889) /gb=NM_017955 /gi=22027508 /ug=Hs.34045 /len=2171	NM_017955	Hs.34045
11414	0.04655	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=NM_002635 /gi=4505774 /ug=Hs.78713 /len=1330	NM_002635	Hs.78713
2177	0.04655	RAB34, member RAS oncogene family (RAB34), mRNA /cds=(206,985) /gb=NM_031934 /gi=21361998 /ug=Hs.301853 /len=1340	NM_031934	Hs.301853
2682	0.04655	choline phosphotransferase 1 (CHPT1), mRNA /cds=(171,1391) /gb=NM_020244 /gi=9910383 /ug=Hs.171889 /len=1536	NM_020244	Hs.171889
9925	0.04655	Similar to vesicle-associated membrane protein 3, clone MGC:2110 IMAGE:3544610, mRNA, complete cds	BC003570	Hs.66708
2164	0.04655	KIAA1074 protein (KIAA1074), mRNA /cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360	NM_014915	Hs.129218
9446	0.04655	hypothetical protein RP1-317E23 (LOC56181), mRNA /cds=(311,1189) /gb=NM_019557 /gi=24475811 /ug=Hs.323396 /len=2119	NM_019557	Hs.323396
2448	0.04655	no match		
3356	0.04655	fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), mRNA /cds=(57,1316) /gb=NM_000137 /gi=4557586 /ug=Hs.73875 /len=1447	NM_000137	Hs.73875
3629	0.04655	hypothetical protein FLJ10707 (FLJ10707), mRNA /cds=(192,2966) /gb=NM_018187 /gi=8922606 /ug=Hs.7187 /len=3334	NM_018187	Hs.7187

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
10393	0.04655	DNA sequence from clone RP5-1116C7 on chromosome 1q24.1-25.1 Contains part of a gene for a protein similar to dynamin, ESTs, STSs, GSSs, complete sequence	AL137157	
10515	0.04655	601656905R1 NIH_MGC_67 cDNA clone IMAGE:3865824 3', mRNA sequence /clone=IMAGE:3865824 /clone_end=3' /gb=BE963107 /gi=11766525 /ug=Hs.418837 /len=800	BE963107	Hs.418837
3231	0.04655	cDNA FLJ39084 fis, clone NT2RP7018871. /cds=(491,1024) /gb=AK096403 /gi=21755888 /ug=Hs.356835 /len=2242	AK096403	Hs.356835
13597	0.04655	wl29b01.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2426281 3', mRNA sequence /clone=IMAGE:2426281 /clone_end=3' /gb=AI866284 /gi=5530391 /ug=Hs.229525 /len=237	AI866284	Hs.229525
7328	0.04655	basic leucine zipper and W2 domains 1 (BZW1), mRNA /cds=(81,1340) /gb=NM_014670 /gi=7661849 /ug=Hs.155291 /len=2998	NM_014670	Hs.155291
4179	0.04655	CD109 (CD109), mRNA /cds=(113,4450) /gb=NM_133493 /gi=19424129 /ug=Hs.55964 /len=5883	NM_133493	Hs.55964
6916	0.04655	cDNA FLJ11174 fis, clone PLACE1007367. /gb=AK002036 /gi=7023674 /ug=Hs.24359 /len=2285	AK002036	Hs.24359
354	0.04655	stromal cell-derived factor 2 (SDF2), mRNA /cds=(40,675) /gb=NM_006923 /gi=14141194 /ug=Hs.118684 /len=1075	NM_006923	Hs.118684
825	0.04655	thioredoxin-like 2 (TXNL2), mRNA /cds=(5,1012) /gb=NM_006541 /gi=5730103 /ug=Hs.42644 /len=1942	NM_006541	Hs.42644
7388	0.04655	ring-box 1 (RBX1), mRNA /cds=(19,345) /gb=NM_014248 /gi=22091459 /ug=Hs.279919 /len=521	NM_014248	Hs.279919
14453	0.04655	no match		
9006	0.04655	cDNA FLJ38383 fis, clone FEBRA2003726. /gb=AK095702 /gi=21755022 /ug=Hs.433517 /len=3240	AK095702	Hs.433517
4502	0.04655	origin recognition complex, subunit 3-like (yeast) (ORC3L), mRNA /cds=(27,2162) /gb=NM_012381 /gi=6912561 /ug=Hs.74420 /len=2510	NM_012381	Hs.74420
1867	0.04655	excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D) (ERCC2), mRNA /cds=(1,2283) /gb=NM_000400 /gi=15834616 /ug=Hs.99987 /len=2318	NM_000400	Hs.99987
1930	0.04655	Smcy Y chromosome (mouse) (SMCY), mRNA /cds=(276,4895) /gb=NM_004653 /gi=4759149 /ug=Hs.80358 /len=5476	NM_004653	Hs.80358
6508	0.046547	osteomodulin (OMD), mRNA /cds=(101,1366) /gb=NM_005014 /gi=4826875 /ug=Hs.94070 /len=2263	NM_005014	Hs.94070

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3315	0.045352	mRNA; cDNA DKFZp667O0320 (from clone DKFZp667O0320) /gb=AL833655 /gi=21734303 /ug=Hs.57847 /len=3543	AL833655	Hs.57847
6773	0.044186	hypothetical protein FLJ14834 (FLJ14834), mRNA /cds=(326,1237) /gb=NM_032849 /gi=21361885 /ug=Hs.62905 /len=2342	NM_032849	Hs.62905
2892	0.044186	t-complex 1 (TCP1), mRNA /cds=(22,1692) /gb=NM_030752 /gi=13540472 /ug=Hs.4112 /len=2019	NM_030752	Hs.4112
14633	0.044186	DNA sequence from clone RP11-22011 on chromosome 9, complete sequence	AL512604	
8189	0.044186	hypothetical protein FLJ14566 (FLJ14566), mRNA /cds=(447,1763) /gb=NM_032806 /gi=21314765 /ug=Hs.12313 /len=2240	NM_032806	Hs.12313
3615	0.044186	mammalian inositol hexakisphosphate kinase 2 (IP6K2), mRNA /cds=(147,1427) /gb=NM_016291 /gi=7705552 /ug=Hs.323432 /len=1737	NM_016291	Hs.323432
11149	0.044186	chromosome 5 clone CTB-113P19, complete sequence	AC011374	
5290	0.044186	hypothetical protein FLJ20719 (FLJ20719), mRNA /cds=(402,2213) /gb=NM_017940 /gi=24308174 /ug=Hs.446473 /len=3745	NM_017940	Hs.446473
2048	0.044186	mRNA for KIAA0701 protein, partial cds. /cds=(1,4065) /gb=AB014601 /gi=20521136 /ug=Hs.153293 /len=4625	AB014601	Hs.153293
9041	0.044186	7140g01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:3524136 3', mRNA sequence /clone=IMAGE:3524136 /clone_end=3' /gb=BF112131 /gi=10941821 /ug=Hs.288083 /len=620	BF112131	Hs.288083
7669	0.044186	hypothetical protein MGC3180 (MGC3180), mRNA /cds=(76,768) /gb=NM_024041 /gi=13128997 /ug=Hs.250570 /len=846	NM_024041	Hs.250570
12744	0.044186	ribosomal protein L15 (RPL15), mRNA /cds=(37,651) /gb=NM_002948 /gi=15431292 /ug=Hs.74267 /len=2018	NM_002948	Hs.74267
6290	0.044186	mRNA; cDNA DKFZp547C1510 (from clone DKFZp547C1510) /gb=AL831873 /gi=21732367 /ug=Hs.377056 /len=2405	AL831873	Hs.377056
3738	0.044186	PDX1 gene for lipoyl-containing component X, exons 1-11	AJ298105	
6169	0.044186	interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA /cds=(238,639) /gb=NM_021034 /gi=11995467 /ug=Hs.381234 /len=808	NM_021034	Hs.381234
4144	0.044186	cDNA FLJ34029 fis, clone FCBBF2003636. /gb=AK091348 /gi=21749698 /ug=Hs.25545 /len=2194	AK091348	Hs.25545
2402	0.044186	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (AKR7A2), mRNA /cds=(78,1070) /gb=NM_003689 /gi=4502020 /ug=Hs.6980 /len=1331	NM_003689	Hs.6980

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Spot	p-value	Description	Accession	Unigene
4934	0.044186	cDNA: FLJ21962 fis, clone HEP05564. /gb=AK025615 /gi=10438186 /ug=Hs.7567 /len=3323	AK025615	Hs.7567
3068	0.044186	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424 /len=6735	NM_013989	Hs.154424
4554	0.044186	integral membrane protein 2B (ITM2B), mRNA /cds=(171,971) /gb=NM_021999 /gi=11527401 /ug=Hs.239625 /len=1843	NM_021999	Hs.239625
2684	0.044186	squalene epoxidase (SQLE), mRNA /cds=(215,1939) /gb=NM_003129 /gi=6806899 /ug=Hs.71465 /len=2277	NM_003129	Hs.71465
772	0.044186	DNA sequence from clone CTA-503F6 on chromosome 22q11.2-12.1, complete sequence	AL021153	
13745	0.044186	protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA /cds=(154,5892) /gb=NM_002839 /gi=4506308 /ug=Hs.158112 /len=6263	NM_002839	Hs.158112
767	0.044183	NADPH oxidase 4 (NOX4), mRNA /cds=(240,1976) /gb=NM_016931 /gi=20149638 /ug=Hs.93847 /len=2416	NM_016931	Hs.93847
12856	0.041922	cDNA FLJ33798 fis, clone CTONG2000063. /gb=AK091117 /gi=21749410 /ug=Hs.7921 /len=3551	AK091117	Hs.7921
3701	0.041922	nudix (nucleoside diphosphate linked moiety X)-type motif 9 (NUDT9), mRNA /cds=(326,1378) /gb=NM_024047 /gi=20127621 /ug=Hs.301789 /len=1718	NM_024047	Hs.301789
4106	0.041922	pre-B-cell colony-enhancing factor (PBEF), mRNA /cds=(28,1503) /gb=NM_005746 /gi=5031976 /ug=Hs.239138 /len=2376	NM_005746	Hs.239138
12383	0.041922	Saccharomyces cerevisiae chromosome XII, complete chromosome sequence	NC_001144	
11276	0.041922	FLN29 gene product (FLN29), mRNA /cds=(55,1803) /gb=NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618	NM_006700	Hs.5148
12932	0.041922	RC1-HT0598-310300-012-d02 HT0598 cDNA, mRNA sequence /gb=BE177770 /gi=8656922 /ug=Hs.292103 /len=437	BE177770	Hs.292103
14494	0.041922	DNA sequence from clone RP11-460N11 on chromosome 9, complete sequence	AL359955	
2943	0.041922	cDNA FLJ31750 fis, clone NT2RI2007406. /gb=AK056312 /gi=16551677 /ug=Hs.27048 /len=1882	AK056312	Hs.27048
2896	0.041922	Danio rerio, clone IMAGE:5914856, mRNA, partial cds	BC049491	Dr.25294
2922	0.041922	ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA /cds=(70,735) /gb=NM_003349 /gi=15718757 /ug=Hs.75875 /len=2394	NM_003349	Hs.75875
2615	0.041922	major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(16,1116) /gb=NM_002117 /gi=19557676 /ug=Hs.277477 /len=1549	NM_002117	Hs.277477

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6363	0.041922	RAS, dexamethasone-induced 1 (RASD1), mRNA /cds=(213,1058) /gb=NM_016084 /gi=22027484 /ug=Hs.25829 /len=1758	NM_016084	Hs.25829
2769	0.041922	GTP binding protein overexpressed in skeletal muscle (GEM), mRNA /cds=(214,1104) /gb=NM_005261 /gi=4885262 /ug=Hs.79022 /len=2156	NM_005261	Hs.79022
5869	0.041922	ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA /cds=(1,3756) /gb=NM_005603 /gi=5031696 /ug=Hs.406187 /len=3756	NM_005603	Hs.406187
2266	0.041922	Yes-associated protein 1, 65kDa (YAP1), mRNA /cds=(250,1614) /gb=NM_006106 /gi=20986484 /ug=Hs.84520 /len=5128	NM_006106	Hs.84520
11288	0.041922	KIAA0563-related gene (LOC114659), mRNA /cds=(1,2841) /gb=NM_052888 /gi=16418400 /ug=Hs.367593 /len=3017	NM_052888	Hs.367593
10936	0.041922	UI-E-EJ1-ajx-e-17-0-UI.r1 UI-E-EJ1 cDNA clone UI-E-EJ1-ajx-e-17-0-UI 5', mRNA sequence /clone=UI-E-EJ1-ajx-e-17-0-UI /clone_end=5' /gb=BQ188692 /gi=20364243 /ug=Hs.76561 /len=1079	BQ188692	Hs.76561
3130	0.041922	unc-84 A (C. elegans) (UNC84A), mRNA	XM_291219	
4457	0.039754	ras gene family, member A (ARHA), mRNA /cds=(152,733) /gb=NM_001664 /gi=10835048 /ug=Hs.77273 /len=1777	NM_001664	Hs.77273
14013	0.039754	chromosome 17, clone RP11-697E22, complete sequence	AC091199	
4887	0.039754	mRNA; cDNA DKFZp434N079 (from clone DKFZp434N079) /gb=AL133591 /gi=6599179 /ug=Hs.141480 /len=1965	AL133591	Hs.141480
2236	0.039754	glia maturation factor, gamma (GMFG), mRNA /cds=(5,433) /gb=NM_004877 /gi=4758439 /ug=Hs.5210 /len=561	NM_004877	Hs.5210
14449	0.039754	clone 25023 mRNA sequence /gb=AF131817 /gi=4406652 /ug=Hs.90858 /len=1466	AF131817	Hs.90858
14366	0.039754	AGENCOURT_6445425 NIH_MGC_72 cDNA clone IMAGE:5540163 5', mRNA sequence /clone=IMAGE:5540163 /clone_end=5' /gb=BM464113 /gi=18513155 /ug=Hs.24808 /len=1069	BM464113	Hs.24808
4268	0.039754	reticulon 3 (RTN3), mRNA /cds=(125,835) /gb=NM_006054 /gi=5174654 /ug=Hs.252831 /len=2524	NM_006054	Hs.252831
4166	0.039754	ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds /cds=(153,1220) /gb=AF022789 /gi=3220153 /ug=Hs.42400 /len=4348	AF022789	Hs.42400
14124	0.039754	Werner helicase interacting protein (WHIP), transcript variant 1, mRNA /cds=(192,2189) /gb=NM_020135 /gi=18426901 /ug=Hs.236828 /len=2670	NM_020135	Hs.236828

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11952	0.039754	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (SMARCA5), mRNA /cds=(463,3621) /gb=NM_003601 /gi=21071057 /ug=Hs.9456 /len=3866	NM_003601	Hs.9456
13408	0.039754	no match		
2904	0.039754	vacuolar protein sorting 26 (yeast) (VPS26), mRNA /cds=(80,1063) /gb=NM_004896 /gi=17978518 /ug=Hs.67052 /len=2652	NM_004896	Hs.67052
10358	0.039754	3 BAC RP11-669C7 (Roswell Park Cancer Institute BAC Library) complete sequence	AC117467	
12690	0.039754	protein transport protein SEC61 alpha subunit isoform 1 (SEC61A1), mRNA /cds=(185,1615) /gb=NM_013336 /gi=14591931 /ug=Hs.306079 /len=3655	NM_013336	Hs.306079
7286	0.039754	mRNA; cDNA DKFZp451D112 (from clone DKFZp451D112); complete cds /cds=(316,4719) /gb=AL831962 /gi=21732493 /ug=Hs.202949 /len=5391	AL831962	Hs.202949
11488	0.039754	preproenkephalin precursor (PEN) gene, exon 3 and complete cds	J00123	
10542	0.03768	mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112) /gb=AL049987 /gi=4884238 /ug=Hs.166361 /len=1215	AL049987	Hs.166361
5665	0.03768	golgi associated, gamma adaptin ear containing, ARF binding protein 3 (GGA3), transcript variant long, mRNA /cds=(10,2181) /gb=NM_138619 /gi=20336266 /ug=Hs.87726 /len=3860	NM_138619	Hs.87726
10857	0.03768	LOC342511 (LOC342511), mRNA	XM_296908	
5093	0.03768	mRNA; cDNA DKFZp434H247 (from clone DKFZp434H247) /cds=(1,638) /gb=AL137304 /gi=6807768 /ug=Hs.164649 /len=3539	AL137304	Hs.164649
12211	0.03768	BAC clone RP11-648L18 from 7, complete sequence	AC069292	
10204	0.03768	BX109229 NCI_CGAP_GCB1 cDNA clone IMAGp998K073291, mRNA sequence /clone=IMAGp998K073291_ IMAGE:1306110 /gb=BX109229 /gi=27835680 /ug=Hs.136841 /len=468	BX109229	Hs.136841
6585	0.03768	R3H domain (binds single-stranded nucleic acids) containing (R3HDM), mRNA /cds=(383,3298) /gb=NM_015361 /gi=7661873 /ug=Hs.268053 /len=4272	NM_015361	Hs.268053
6128	0.03768	Rab acceptor 1 (prenylated) (RABAC1), mRNA /cds=(31,588) /gb=NM_006423 /gi=5453959 /ug=Hs.11417 /len=770	NM_006423	Hs.11417
11858	0.03768	LOC284512 (LOC284512), mRNA	XM_211500	
6854	0.03768	mRNA; cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds /cds=(1,476) /gb=AL122071 /gi=6102868 /ug=Hs.238927 /len=2499	AL122071	Hs.238927

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5768	0.03768	high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 1, mRNA /cds=(179,478) /gb=NM_004242 /gi=23238229 /ug=Hs.77558 /len=935	NM_004242	Hs.77558
14486	0.03768	BAC clone RP11-379A15 from 2, complete sequence	AC114765	
14364	0.03768	clone IMAGE:3446533, mRNA /gb=BC013214 /gi=15301467 /ug=Hs.404874 /len=2076	BC013214	Hs.404874
14169	0.03768	UI-H-EI0-ayg-o-16-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-ayg-o-16-0-UI 3', mRNA sequence /clone=UI-H-EI0-ayg-o-16-0-UI /clone_end=3' /gb=CA449027 /gi=24813447 /ug=Hs.44888 /len=573	CA449027	Hs.44888
1274	0.03768	HSJ1a (HSJ1) mRNA, complete cds; alternatively spliced. /cds=(26,859) /gb=S37375 /gi=250081 /ug=Hs.433237 /len=1760	S37375	Hs.433237
12253	0.03768	cDNA FLJ12534 fis, clone NT2RM4000244. /gb=AK022596 /gi=10434077 /ug=Hs.108646 /len=2425	AK022596	Hs.108646
6618	0.03768	eukaryotic translation elongation factor 1 gamma (EEF1G), mRNA /cds=(38,1351) /gb=NM_001404 /gi=25453475 /ug=Hs.256184 /len=1429	NM_001404	Hs.256184
4199	0.03768	protein phosphatase 1, regulatory subunit 10 (PPP1R10), mRNA /cds=(553,3375) /gb=NM_002714 /gi=25777670 /ug=Hs.106019 /len=4540	NM_002714	Hs.106019
10040	0.037677	frizzled 8 (Drosophila) (FZD8), mRNA /cds=(6,2090) /gb=NM_031866 /gi=13994189 /ug=Hs.302634 /len=3195	NM_031866	Hs.302634
3020	0.035696	hypothetical protein DJ667H12.2 (DJ667H12.2), mRNA /cds=(180,1250) /gb=NM_019605 /gi=19923818 /ug=Hs.21068 /len=2038	NM_019605	Hs.21068
6431	0.035696	hypothetical protein FLJ10134 (FLJ10134), mRNA /cds=(314,1141) /gb=NM_018004 /gi=8922242 /ug=Hs.104800 /len=1564	NM_018004	Hs.104800
6906	0.035696	polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA /cds=(79,462) /gb=NM_021974 /gi=14602451 /ug=Hs.46405 /len=546	NM_021974	Hs.46405
13261	0.035696	B aggressive lymphoma gene (BAL), mRNA /cds=(229,2793) /gb=NM_031458 /gi=13899296 /ug=Hs.47783 /len=3243	NM_031458	Hs.47783
13338	0.035696	solute carrier family 30 (zinc transporter), member 5 (SLC30A5), mRNA /cds=(202,2499) /gb=NM_022902 /gi=20070322 /ug=Hs.129445 /len=2952	NM_022902	Hs.129445
13353	0.035696	transcription termination factor-like protein (LOC80298), mRNA /cds=(341,1498) /gb=NM_025198 /gi=21314735 /ug=Hs.5009 /len=1792	NM_025198	Hs.5009
479	0.035696	SNF-1 related kinase (SNRK), mRNA /cds=(642,2939) /gb=NM_017719 /gi=21361642 /ug=Hs.79025 /len=5519	NM_017719	Hs.79025
859	0.035696	yippee protein (CGI-127), mRNA /cds=(126,491) /gb=NM_016061 /gi=7706340 /ug=Hs.184542 /len=2183	NM_016061	Hs.184542

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
14800	0.035696	UI-H-FH0-bcj-p-06-0-UI.s1 NCI_CGAP_FH0 cDNA clone UI-H-FH0-bcj-p-06-0-UI 3', mRNA sequence /clone=UI-H-FH0-bcj-p-06-0-UI /clone_end=3' /gb=BQ775499 /gi=21983975 /ug=Hs.442354 /len=1070	BQ775499	Hs.442354
7342	0.035696	KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NM_015208 /gi=14140237 /ug=Hs.27973 /len=6189	NM_015208	Hs.27973
14655	0.035696	AGENCOURT_6758988 NIH_MGC_115 cDNA clone IMAGE:5755234 5', mRNA sequence /clone=IMAGE:5755234 /clone_end=5' /gb=BQ067651 /gi=19896697 /ug=Hs.204354 /len=1385	BQ067651	Hs.204354
14435	0.035693	chromosome 17, clone RP11-44H5, complete sequence	AC007982	
6701	0.0338	inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA	NM_002223	
2317	0.0338	mRNA for KIAA0570 protein, partial cds. /cds=(480,10718) /gb=AB011142 /gi=20521084 /ug=Hs.180948 /len=11269	AB011142	Hs.180948
4108	0.0338	chromosome 15 clone RP11-139H15 map 15q21.3, complete sequence	AC018926	
7274	0.0338	cDNA: FLJ21208 fis, clone COL00363. /gb=AK024861 /gi=10437269 /ug=Hs.289007 /len=1999	AK024861	Hs.289007
1653	0.0338	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 /len=753	NM_021130	Hs.401787
8197	0.0338	mRNA for KIAA1013 protein, partial cds. /cds=(1,3189) /gb=AB023230 /gi=4589675 /ug=Hs.96427 /len=4783	AB023230	Hs.96427
6639	0.0338	cDNA: FLJ20935 fis, clone ADSE01534	AK024588	Hs.25253
2840	0.0338	KIAA0040 gene product (KIAA0040), mRNA /cds=(921,1382) /gb=NM_014656 /gi=7657258 /ug=Hs.158282 /len=4564	NM_014656	Hs.158282
10780	0.0338	hypothetical protein FLJ10300 (FLJ10300), mRNA /cds=(1710,3359) /gb=NM_018051 /gi=21361686 /ug=Hs.42233 /len=3785	NM_018051	Hs.42233
14035	0.0338	hypothetical protein DKFZp434K0427 (DKFZP434K0427), mRNA /cds=(342,1814) /gb=NM_032148 /gi=14149818 /ug=Hs.238996 /len=2375	NM_032148	Hs.238996
6504	0.0338	CED-6 protein (CED-6), mRNA /cds=(429,1343) /gb=NM_016315 /gi=7705317 /ug=Hs.107056 /len=3277	NM_016315	Hs.107056
14644	0.031988	UI-H-DT0-aty-f-17-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5866000 3', mRNA sequence /clone=IMAGE:5866000 /clone_end=3' /gb=BM993116 /gi=19712505 /ug=Hs.433791 /len=1232	BM993116	Hs.433791

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
8319	0.031988	hi41b02.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2974827 3', mRNA sequence /clone=IMAGE:2974827 /clone_end=3' /gb=AW628548 /gi=7375338 /ug=Hs.278113 /len=554	AW628548	Hs.278113
12336	0.031988	UI-H-ED0-axn-i-09-0-UI.s1 NCI_CGAP_ED0 cDNA clone UI-H-ED0-axn-i-09-0-UI 3', mRNA sequence /clone=UI-H-ED0-axn-i-09-0-UI /clone_end=3' /gb=CA445401 /gi=24809821 /ug=Hs.204930 /len=725	CA445401	Hs.204930
6326	0.031988	mitochondrial ribosomal protein S31 (MRPS31), nuclear gene encoding mitochondrial protein, mRNA /cds=(22,1209) /gb=NM_005830 /gi=16950599 /ug=Hs.154655 /len=1284	NM_005830	Hs.154655
3685	0.031988	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1), mRNA /cds=(122,1357) /gb=NM_003079 /gi=21264354 /ug=Hs.332848 /len=1576	NM_003079	Hs.332848
11711	0.031988	EH-domain containing 1 (EHD1), mRNA /cds=(247,1851) /gb=NM_006795 /gi=5803008 /ug=Hs.155119 /len=3508	NM_006795	Hs.155119
10560	0.031988	chromosome 1 clone RP4-802A10, complete sequence	AC096947	
3913	0.031988	hairy and enhancer of split 1, (Drosophila) (HES1), mRNA /cds=(237,1079) /gb=NM_005524 /gi=8400709 /ug=Hs.250666 /len=1471	NM_005524	Hs.250666
9141	0.030258	EST384025 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW972041 /gi=8161782 /ug=Hs.190176 /len=617	AW972041	Hs.190176
6667	0.030258	arginase, type II (ARG2), nuclear gene encoding mitochondrial protein, mRNA /cds=(39,1103) /gb=NM_001172 /gi=10947110 /ug=Hs.172851 /len=1886	NM_001172	Hs.172851
1878	0.030258	capping protein (actin filament), gelsolin-like (CAPG), mRNA /cds=(50,1096) /gb=NM_001747 /gi=4502560 /ug=Hs.82422 /len=1221	NM_001747	Hs.82422
616	0.030258	hypothetical protein FLJ14281 (FLJ14281), mRNA /cds=(442,822) /gb=NM_024920 /gi=13376391 /ug=Hs.266957 /len=2303	NM_024920	Hs.266957
13846	0.030258	RTC domain containing 1 (RTCD1), mRNA /cds=(171,1271) /gb=NM_003729 /gi=4506588 /ug=Hs.27076 /len=1539	NM_003729	Hs.27076
13673	0.030258	KIAA1128 protein (KIAA1128), mRNA /cds=(553,2253) /gb=NM_018999 /gi=24308130 /ug=Hs.81897 /len=7248	NM_018999	Hs.81897
1675	0.030258	coagulation factor XIII, A1 polypeptide (F13A1), mRNA /cds=(102,2300) /gb=NM_000129 /gi=9961355 /ug=Hs.80424 /len=3833	NM_000129	Hs.80424

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
9921	0.030258	hypothetical protein FLJ10477 (FLJ10477), mRNA /cds=(232,873) /gb=NM_018105 /gi=8922445 /ug=Hs.7432 /len=2167	NM_018105	Hs.7432
9883	0.030258	chromosome 11 open reading frame2 (C11orf2), mRNA	NM_013265	Hs.5258
2092	0.030258	cAMP-regulated guanine nucleotide exchange factor II (CAMP-GEFII), mRNA /cds=(109,3144) /gb=NM_007023 /gi=5901913 /ug=Hs.91971 /len=4278	NM_007023	Hs.91971
12447	0.030258	cDNA FLJ12049 fis, clone HEMBB1001996. /gb=AK022111 /gi=10433434 /ug=Hs.171395 /len=2100	AK022111	Hs.171395
14643	0.030258	UI-H-FG1-bgh-l-12-0-UI.s1 NCI_CGAP_FG1 cDNA clone UI-H-FG1-bgh-l-12-0-UI 3', mRNA sequence /clone=UI-H-FG1-bgh-l-12-0-UI /clone_end=3' /gb=BU624037 /gi=23290252 /ug=Hs.416904 /len=1160	BU624037	Hs.416904
4656	0.030258	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa (TAF9), transcript variant 1, mRNA /cds=(159,953) /gb=NM_003187 /gi=21166375 /ug=Hs.60679 /len=1153	NM_003187	Hs.60679
12202	0.030258	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540
3161	0.030258	hypothetical protein DRAPC1 (DRAPC1), mRNA /cds=(354,1898) /gb=NM_153000 /gi=23308596 /ug=Hs.374481 /len=2572	NM_153000	Hs.374481
5208	0.030258	transforming growth factor, beta-induced, 68kDa (TGFB1), mRNA /cds=(48,2099) /gb=NM_000358 /gi=4507466 /ug=Hs.118787 /len=2691	NM_000358	Hs.118787
5751	0.030258	serine/arginine repetitive matrix 1 (SRRM1), mRNA /cds=(6,2468) /gb=NM_005839 /gi=5032118 /ug=Hs.18192 /len=3698	NM_005839	Hs.18192
3254	0.028607	splicing factor, arginine/serine-rich 2 (SF2SF2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965
10818	0.028607	hypothetical protein FLJ20156 (FLJ20156), mRNA /cds=(248,2305) /gb=NM_017691 /gi=8923153 /ug=Hs.12692 /len=2780	NM_017691	Hs.12692
12960	0.028607	hypothetical protein FLJ25157 (FLJ25157), mRNA /cds=(157,762) /gb=NM_152653 /gi=22749326 /ug=Hs.108323 /len=1541	NM_152653	Hs.108323
344	0.028607	tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA /cds=(77,910) /gb=NM_007115 /gi=26051242 /ug=Hs.29352 /len=1440	NM_007115	Hs.29352
5435	0.028607	prolylcarboxypeptidase (angiotensinase C) (PRCP), mRNA /cds=(30,1520) /gb=NM_005040 /gi=4826939 /ug=Hs.75693 /len=2060	NM_005040	Hs.75693
12342	0.028607	clone IMAGE:3909104, mRNA /gb=BC015719 /gi=16041698 /ug=Hs.8852 /len=3169	BC015719	Hs.8852

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
4003	0.028607	methylmalonyl CoA epimerase (MCEE), mRNA /cds=(11,541) /gb=NM_032601 /gi=21314761 /ug=Hs.94949 /len=850	NM_032601	Hs.94949
13375	0.028607	neurocalcin delta (NCALD), mRNA /cds=(121,702) /gb=NM_032041 /gi=14042973 /ug=Hs.90063 /len=3300	NM_032041	Hs.90063
1506	0.027032	septin 2 (SEP2) mRNA, partial cds /cds=(1,1528) /gb=AF179995 /gi=9957543 /ug=Hs.80712 /len=4344	AF179995	Hs.80712
6668	0.027032	mitochondrion, complete genome	NC_001807	
12481	0.027032	BAC clone RP11-738E22 from 4, complete sequence	AC069307	
14194	0.027032	th01b07.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2116981 3' similar to gb:J03626 URIDINE 5'-MONOPHOSPHATE SYNTHASE mRNA sequence /clone=IMAGE:2116981 /clone_end=3' /gb=AI524056 /gi=4438191 /ug=Hs.369101 /len=475	AI524056	Hs.369101
14336	0.027032	chromosome 15, clone RP11-236J21, complete sequence	AC090179	
13159	0.027032	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (ECHS1), nuclear gene encoding mitochondrial protein, mRNA /cds=(72,944) /gb=NM_004092 /gi=12707569 /ug=Hs.76394 /len=1326	NM_004092	Hs.76394
6105	0.027032	retinoblastoma binding protein 6 (RBBP6), mRNA /cds=(92,2938) /gb=NM_006910 /gi=5902043 /ug=Hs.91065 /len=2994	NM_006910	Hs.91065
13198	0.027032	602143541F1 NIH_MGC_46 cDNA clone IMAGE:4304530 5', mRNA sequence /clone=IMAGE:4304530 /clone_end=5' /gb=BF686613 /gi=11972021 /ug=Hs.31387 /len=1347	BF686613	Hs.31387
14376	0.027032	UI-H-EU0-azl-k-15-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE: 5850374 3', mRNA sequence /clone=IMAGE: 5850374 /clone_end=3' /gb=BQ181216 /gi=20356708 /ug=Hs.442170 /len=1044	BQ181216	Hs.442170
2974	0.027032	adipose differentiation-related protein, clone MGC:10598 IMAGE:3844174, mRNA, complete cds	BC005127	Hs.3416
2621	0.027032	IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(468,5441) /gb=NM_003870 /gi=4506786 /ug=Hs.1742 /len=7573	NM_003870	Hs.1742
5874	0.027032	BX104663 Soares_pregnant_uterus_NbHPU cDNA clone IMAGp998J071170, mRNA sequence /clone=IMAGp998J071170; IMAGE:491622 /gb=BX104663 /gi=27846238 /ug=Hs.426388 /len=748	BX104663	Hs.426388
6362	0.027032	inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA /cds=(99,932) /gb=NM_005536 /gi=8393607 /ug=Hs.171776 /len=2349	NM_005536	Hs.171776
13124	0.027032	complement component 5 (C5), mRNA /cds=(13,5043) /gb=NM_001735 /gi=4502506 /ug=Hs.1281 /len=5444	NM_001735	Hs.1281

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
2849	0.027032	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627	NM_004894	Hs.109052
5962	0.027032	ubiquitin-conjugating enzyme E2L 6 (UBE2L6), mRNA /cds=(48,509) /gb=NM_004223 /gi=4759281 /ug=Hs.425777 /len=1223	NM_004223	Hs.425777
1081	0.02553	glutaredoxin (thioltransferase) (GLRX), mRNA /cds=(16,336) /gb=NM_002064 /gi=4504024 /ug=Hs.28988 /len=1328	NM_002064	Hs.28988
7710	0.02553	cDNA: FLJ21531 fis, clone COL06036. /gb=AK025184 /gi=10437647 /ug=Hs.102941 /len=2671	AK025184	Hs.102941
7659	0.02553	ubiquitination factor E4B (UFD2 yeast) (UBE4B), mRNA /cds=(86,3994) /gb=NM_006048 /gi=5174482 /ug=Hs.24594 /len=5314	NM_006048	Hs.24594
254	0.02553	cytoplasmic FMR1 interacting protein 1 (CYFIP1), mRNA /cds=(53,3814) /gb=NM_014608 /gi=24307968 /ug=Hs.77257 /len=4394	NM_014608	Hs.77257
9780	0.02553	arrestin, beta 2 (ARRB2), mRNA /cds=(234,1463) /gb=NM_004313 /gi=21626464 /ug=Hs.18142 /len=1941	NM_004313	Hs.18142
5847	0.02553	clone IMAGE:5286336, mRNA /gb=BC043158 /gi=27693197 /ug=Hs.434381 /len=2786	BC043158	Hs.434381
11400	0.02553	leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782	NM_133259	Hs.182490
12457	0.02553	chromosome 18, clone RP11-268I9, complete sequence	AC103987	
2554	0.02553	chromodomain helicase DNA binding protein 1 (CHD1), mRNA /cds=(164,5293) /gb=NM_001270 /gi=4557446 /ug=Hs.22670 /len=5947	NM_001270	Hs.22670
6259	0.02553	transducin (beta)-like 2 (TBL2), transcript variant 2, mRNA /cds=(95,322) /gb=NM_032988 /gi=14670378 /ug=Hs.52515 /len=2494	NM_032988	Hs.52515
6388	0.02553	mago-nashi proliferation-associated (Drosophila) (MAGOH), mRNA /cds=(89,529) /gb=NM_002370 /gi=6006021 /ug=Hs.57904 /len=698	NM_002370	Hs.57904
2551	0.02553	protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), mRNA /cds=(259,1242) /gb=NM_002709 /gi=4506004 /ug=Hs.21537 /len=3590	NM_002709	Hs.21537
8932	0.02553	PTEN induced putative kinase 1 (PINK1), mRNA /cds=(95,1840) /gb=NM_032409 /gi=14165271 /ug=Hs.6163 /len=2700	NM_032409	Hs.6163
284	0.0241	translin-associated factor X (TSNAX), mRNA /cds=(159,1031) /gb=NM_005999 /gi=20302159 /ug=Hs.96247 /len=2667	NM_005999	Hs.96247
6540	0.0241	LIM and SH3 protein 1 (LASP1), mRNA /cds=(76,861) /gb=NM_006148 /gi=5453709 /ug=Hs.334851 /len=3846	NM_006148	Hs.334851
11872	0.0241	FUS interacting protein (serine-arginine rich) 1 (FUSIP1), transcript variant 1, mRNA	NM_006625	Hs.3530

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
4662	0.0241	CGI-128 protein (CGI-128), mRNA /cds=(36,527) /gb=NM_016062 /gi=7706342 /ug=Hs.9825 /len=670	NM_016062	Hs.9825
2701	0.0241	epilepsy, progressive myoclonus type 2; Lafora disease (laforin) (EPM2A), mRNA /cds=(358,1353) /gb=NM_005670 /gi=20127480 /ug=Hs.22464 /len=3487	NM_005670	Hs.22464
7890	0.0241	likely ortholog of Xenopus dullard (HSA011916), mRNA /cds=(31,765) /gb=NM_015343 /gi=7661721 /ug=Hs.84359 /len=1356	NM_015343	Hs.84359
8199	0.0241	hypothetical protein MGC18216 (MGC18216), mRNA /cds=(2207,2374) /gb=NM_152452 /gi=22748948 /ug=Hs.104679 /len=3270	NM_152452	Hs.104679
147	0.0241	hypothetical protein FLJ12799 (FLJ12799), mRNA /cds=(485,1324) /gb=NM_022495 /gi=22095362 /ug=Hs.22549 /len=1926	NM_022495	Hs.22549
4979	0.0241	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045
3815	0.023408	no match		
11722	0.022737	retinol binding protein 1, cellular (RBP1), mRNA /cds=(126,533) /gb=NM_002899 /gi=8400726 /ug=Hs.101850 /len=720	NM_002899	Hs.101850
10431	0.022737	UI-E-EJ0-ahk-j-14-0-UI.r2 UI-E-EJ0 cDNA clone UI-E-EJ0-ahk-j-14-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahk-j-14-0-UI /clone_end=5' /gb=BM716760 /gi=19030018 /ug=Hs.381096 /len=1042	BM716760	Hs.381096
5625	0.022737	opioid growth factor receptor (OGFR), mRNA /cds=(206,2062) /gb=NM_007346 /gi=6671492 /ug=Hs.67896 /len=2423	NM_007346	Hs.67896
1504	0.022737	myeloid cell leukemia sequence 1 (BCL2-related) (MCL1), mRNA /cds=(64,1116) /gb=NM_021960 /gi=19923213 /ug=Hs.86386 /len=3953	NM_021960	Hs.86386
6381	0.022737	hypothetical protein FLJ20580 (FLJ20580), mRNA /cds=(43,525) /gb=NM_017887 /gi=8923540 /ug=Hs.146861 /len=1118	NM_017887	Hs.146861
2129	0.022737	cDNA FLJ31438 fis, clone NT2NE2000706	AK056000	Hs.24423
2059	0.022737	hypothetical protein FLJ20337 (FLJ20337), mRNA /cds=(148,639) /gb=NM_017772 /gi=8923313 /ug=Hs.26898 /len=2491	NM_017772	Hs.26898
5016	0.022737	ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM_000985 /gi=14591906 /ug=Hs.82202 /len=898	NM_000985	Hs.82202
2813	0.022737	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290
14495	0.022737	DNA sequence from clone RP11-15J10 on chromosome 9, complete sequence	AL512605	
13091	0.022737	DNA sequence from clone RP11-236F9 on chromosome 9, complete sequence	AL845321	

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
6837	0.021441	cDNA FLJ39699 fis, clone SMINT2011567, weakly similar to mRNA for ALEX1. /gb=AK097018 /gi=21756651 /ug=Hs.83530 /len=2257	AK097018	Hs.83530
10416	0.021441	Similar to seven in absentia (Drosophila) 2, clone MGC:17169 IMAGE:4153095, mRNA, complete cds	BC013082	Hs.20191
12310	0.021441	602644358F1 NIH_MGC_61 cDNA clone IMAGE:4775006 5', mRNA sequence /clone=IMAGE:4775006 /clone_end=5' /gb=BG615069 /gi=13666440 /ug=Hs.190422 /len=770	BG615069	Hs.190422
2185	0.021441	3 BAC RP11-321F19 (Roswell Park Cancer Institute BAC Library) complete sequence	AC021649	
11280	0.021441	mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624) /gb=AL110152 /gi=5817054 /ug=Hs.94030 /len=1341	AL110152	Hs.94030
5315	0.021441	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=NM_006925 /gi=5902077 /ug=Hs.166975 /len=1865	NM_006925	Hs.166975
591	0.021441	no match		
4883	0.020207	heat shock 105kD (HSP105B), mRNA /cds=(314,2758) /gb=NM_006644 /gi=5729878 /ug=Hs.36927 /len=3448	NM_006644	Hs.36927
8276	0.020207	clone IMAGE:5263917, mRNA /gb=BC035134 /gi=23272887 /ug=Hs.124538 /len=4663	BC035134	Hs.124538
6011	0.020207	clone IMAGE:5260578, mRNA	BC037492	Hs.5518
4676	0.020207	CDA14 (LOC51290), mRNA /cds=(89,1225) /gb=NM_016570 /gi=7706104 /ug=Hs.26813 /len=1378	NM_016570	Hs.26813
205	0.020207	mRNA for KIAA0268 gene, partial cds. /cds=(1,3582) /gb=D87742 /gi=1665824 /ug=Hs.241552 /len=5976	D87742	Hs.241552
10014	0.020207	interferon, alpha-inducible protein 27 (IFI27), mRNA /cds=(55,423) /gb=NM_005532 /gi=5031780 /ug=Hs.278613 /len=597	NM_005532	Hs.278613
6282	0.020207	mesoderm induction early response 1 (MI-ER1), mRNA /cds=(234,1844) /gb=NM_020948 /gi=24308260 /ug=Hs.222746 /len=4972	NM_020948	Hs.222746
14277	0.020207	cDNA FLJ40901 fis, clone UTERU2003704. /gb=AK098220 /gi=21758189 /ug=Hs.44898 /len=2556	AK098220	Hs.44898
12268	0.020207	chromosome 19 clone CTD-2017D11, complete sequence	AC092279	
13307	0.020207	FAD104 (FAD104), mRNA /cds=(58,3672) /gb=NM_022763 /gi=27477058 /ug=Hs.299883 /len=6894	NM_022763	Hs.299883
12646	0.020207	forkhead box P1 (FOXP1), mRNA /cds=(432,2465) /gb=NM_032682 /gi=19923670 /ug=Hs.274344 /len=4954	NM_032682	Hs.274344
6921	0.020207	drebrin 1 (DBN1), transcript variant 2, mRNA /cds=(611,2566) /gb=NM_080881 /gi=18426912 /ug=Hs.89434 /len=3383	NM_080881	Hs.89434

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
4454	0.020207	chromosome 12 open reading frame 8 (C12orf8), mRNA /cds=(12,797) /gb=NM_006817 /gi=13124889 /ug=Hs.75841 /len=963	NM_006817	Hs.75841
13763	0.020207	mutS 6 (E. coli) (MSH6), mRNA /cds=(88,4170) /gb=NM_000179 /gi=4504190 /ug=Hs.3248 /len=4264	NM_000179	Hs.3248
8061	0.020207	mRNA; cDNA DKFZp434J214 (from clone DKFZp434J214); partial cds /cds=(1,1082) /gb=AL080156 /gi=5262614 /ug=Hs.12813 /len=2749	AL080156	Hs.12813
13859	0.020207	Repetitive Sequence		
8168	0.019035	hypothetical protein FLJ23221 (FLJ23221), mRNA /cds=(24,419) /gb=NM_024579 /gi=13375757 /ug=Hs.18397 /len=519	NM_024579	Hs.18397
14363	0.019035	BAC clone RP11-692D12 from 4, complete sequence	AC053527	
6054	0.019035	poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848	NM_002568	Hs.172182
5922	0.019035	proline arginine-rich end leucine-rich repeat protein (PRELP), mRNA /cds=(129,1277) /gb=NM_002725 /gi=4506040 /ug=Hs.76494 /len=1560	NM_002725	Hs.76494
6031	0.019035	ER-resident protein ERdj5 (ERdj5), mRNA /cds=(416,2797) /gb=NM_018981 /gi=24308126 /ug=Hs.1098 /len=4193	NM_018981	Hs.1098
12158	0.019035	PTK2 protein tyrosine kinase 2 (PTK2), transcript variant 1, mRNA /cds=(231,3389) /gb=NM_153831 /gi=27886591 /ug=Hs.740 /len=4453	NM_153831	Hs.740
8543	0.019035	BAC clone RP11-313N8 from 2, complete sequence	AC110926	
6642	0.019035	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), mRNA /cds=(445,1887) /gb=NM_001754 /gi=19923197 /ug=Hs.129914 /len=6212	NM_001754	Hs.129914
13774	0.019035	fetal Alzheimer antigen (FALZ), mRNA /cds=(37,2469) /gb=NM_004459 /gi=6552329 /ug=Hs.99872 /len=2616	NM_004459	Hs.99872
9445	0.017921	barrier to autointegration factor (BCRP1), mRNA /cds=(508,777) /gb=NM_003860 /gi=11038645 /ug=Hs.433759 /len=1192	NM_003860	Hs.433759
7139	0.017921	activated leukocyte cell adhesion molecule (ALCAM), mRNA /cds=(64,1815) /gb=NM_001627 /gi=4502028 /ug=Hs.10247 /len=2539	NM_001627	Hs.10247
11727	0.017921	SUMO-1-specific protease (SUSP1), mRNA /cds=(1,3339) /gb=NM_015571 /gi=7662311 /ug=Hs.27197 /len=4210	NM_015571	Hs.27197
14767	0.017921	chemokine-like factor super family 4 isoform 1 (CKLFSF4) mRNA, complete cds /cds=(183,887) /gb=AF521889 /gi=25167082 /ug=Hs.325825 /len=3430	AF521889	Hs.325825
8788	0.017921	DNA sequence from clone CTA-211L9 on chromosome 6 Contains the gene for KIAA0164 protein, ESTs, STSs, GSSs and CpG Islands, complete sequence	AL121713	

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
3765	0.017921	cold inducible RNA binding protein (CIRBP), mRNA /cds=(81,599) /gb=NM_001280 /gi=4502846 /ug=Hs.119475 /len=1322	NM_001280	Hs.119475
6628	0.017921	CGG triplet repeat binding protein 1 (CGGBP1), mRNA /cds=(357,863) /gb=NM_003663 /gi=21361098 /ug=Hs.86041 /len=4279	NM_003663	Hs.86041
7273	0.017921	interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA /cds=(238,639) /gb=NM_021034 /gi=11995467 /ug=Hs.381234 /len=808	NM_021034	Hs.381234
177	0.017921	chromosome X clone multiple clones map Xp11.23, complete sequence	AF235097	
10305	0.016863	DNA sequence from clone RP11-9819 on chromosome 6, complete sequence	AL513550	
5195	0.016863	angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA /cds=(196,1416) /gb=NM_139314 /gi=21536397 /ug=Hs.9613 /len=1967	NM_139314	Hs.9613
7554	0.016863	mRNA full length insert cDNA clone EUROIMAGE 40627	AL109779	Hs.341203
10342	0.016863	hypothetical protein FLJ38725 (FLJ38725), mRNA /cds=(322,1614) /gb=NM_153218 /gi=23397476 /ug=Hs.210586 /len=2468	NM_153218	Hs.210586
6389	0.016863	annexin A7 (ANXA7), transcript variant 2, mRNA /cds=(61,1527) /gb=NM_004034 /gi=4809278 /ug=Hs.386741 /len=2176	NM_004034	Hs.386741
11056	0.015858	cDNA: FLJ22050 fis, clone HEP09454. /gb=AK025703 /gi=10438305 /ug=Hs.173705 /len=1990	AK025703	Hs.173705
3475	0.015858	hypothetical protein FLJ12389 similar to acetoacetyl-CoA synthetase (FLJ12389), mRNA /cds=(149,2167) /gb=NM_023928 /gi=12965198 /ug=Hs.239758 /len=3253	NM_023928	Hs.239758
13146	0.015858	UI-H-DH0-aui-p-19-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871234 3', mRNA sequence /clone=IMAGE:5871234 /clone_end=3' /gb=BM994422 /gi=19719323 /ug=Hs.289721 /len=2081	BM994422	Hs.289721
2845	0.015858	mRNA for MEGF5, partial cds	AB011538	Hs.57929
3544	0.015858	mRNA for KIAA1999 protein. /cds=(1,3829) /gb=AB082530 /gi=21693143 /ug=Hs.9343 /len=8213	AB082530	Hs.9343
7713	0.015858	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC), mRNA /cds=(337,1875) /gb=NM_005605 /gi=21361289 /ug=Hs.75206 /len=2230	NM_005605	Hs.75206
13332	0.014906	CGI-19 protein (CGI-19), mRNA /cds=(361,1566) /gb=NM_015948 /gi=21361502 /ug=Hs.285847 /len=2068	NM_015948	Hs.285847
10959	0.014906	7p65g03.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3650861 3', mRNA sequence /clone=IMAGE:3650861 /clone_end=3' /gb=BF436898 /gi=11449213 /ug=Hs.213352 /len=426	BF436898	Hs.213352

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
7384	0.014906	RNA helicase (KIAA0801), mRNA /cds=(145,3243) /gb=NM_014829 /gi=7662317 /ug=Hs.17585 /len=3740	NM_014829	Hs.17585
4969	0.014906	mRNA; cDNA DKFZp434A163 (from clone DKFZp434A163); partial cds /cds=(1,4964) /gb=AL110218 /gi=5817150 /ug=Hs.127401 /len=5084	AL110218	Hs.127401
202	0.014906	cytochrome b5 reductase 1 (B5R.1) (CYB5R1), mRNA /cds=(27,944) /gb=NM_016243 /gi=7706454 /ug=Hs.289113 /len=1603	NM_016243	Hs.289113
12394	0.014906	nz21g06.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:1288474 3', mRNA sequence /clone=IMAGE:1288474 /clone_end=3' /gb=AA761475 /gi=2810405 /ug=Hs.291552 /len=363	AA761475	Hs.291552
3034	0.014906	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072
6502	0.014906	DC2 protein (DC2), mRNA /cds=(60,509) /gb=NM_021227 /gi=24308270 /ug=Hs.103180 /len=1090	NM_021227	Hs.103180
10149	0.014906	mRNA; cDNA DKFZp667P1220 (from clone DKFZp667P1220) /gb=AL833656 /gi=21734304 /ug=Hs.280974 /len=5593	AL833656	Hs.280974
13279	0.014906	UI-E-EJ0-ahr-e-11-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahr-e-11-0-UI 3', mRNA sequence /clone=UI-E-EJ0-ahr-e-11-0-UI /clone_end=3' /gb=BU739063 /gi=23676884 /ug=Hs.58668 /len=1345	BU739063	Hs.58668
7769	0.014904	gene for MTG8b, partial cds	AB074982	
13034	0.014002	UI-H-BI2-agj-b-05-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2724417 3', mRNA sequence /clone=IMAGE:2724417 /clone_end=3' /gb=AW290973 /gi=6697609 /ug=Hs.443419 /len=863	AW290973	Hs.443419
3080	0.014002	extracellular link domain containing 1 (XLKD1), mRNA /cds=(91,1059) /gb=NM_006691 /gi=5729910 /ug=Hs.17917 /len=2313	NM_006691	Hs.17917
4942	0.014002	AF034176 mRNA (Tripodis and Ragoussis) cDNA clone ntcon5 contig /gb=AF034176 /gi=2707738 /ug=Hs.188882 /len=7232	AF034176	Hs.188882
3142	0.014002	single-stranded DNA binding protein (SSBP1), mRNA /cds=(79,525) /gb=NM_003143 /gi=4507230 /ug=Hs.923 /len=628	NM_003143	Hs.923
1947	0.014002	transforming, acidic coiled-coil containing protein 1 (TACC1), mRNA /cds=(321,2738) /gb=NM_006283 /gi=5454099 /ug=Hs.173159 /len=7758	NM_006283	Hs.173159
14309	0.013147	wk71e10.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2420874 3', mRNA sequence /clone=IMAGE:2420874 /clone_end=3' /gb=AI815141 /gi=5426356 /ug=Hs.230542 /len=357	AI815141	Hs.230542

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
4807	0.013147	glypican 6 (GPC6), mRNA /cds=(616,2283) /gb=NM_005708 /gi=8051601 /ug=Hs.118407 /len=2760	NM_005708	Hs.118407
6818	0.013147	midline 1 fetal kidney isoform 3 (MID1) mRNA, partial cds	AF041210	Hs.27695
8081	0.012336	TBP-interacting protein (TIP120A), mRNA /cds=(350,4042) /gb=NM_018448 /gi=21361793 /ug=Hs.184786 /len=5387	NM_018448	Hs.184786
13711	0.012336	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679
5049	0.012336	mRNA for KIAA0592 protein, partial cds. /cds=(1,4062) /gb=AB011164 /gi=3043707 /ug=Hs.439367 /len=4623	AB011164	Hs.439367
9920	0.01157	hypothetical protein FLJ22419 (FLJ22419), mRNA /cds=(409,1596) /gb=NM_024697 /gi=13375980 /ug=Hs.99256 /len=1674	NM_024697	Hs.99256
482	0.01157	myosin binding protein H (MYBPH), mRNA /cds=(29,1459) /gb=NM_004997 /gi=4826841 /ug=Hs.927 /len=1772	NM_004997	Hs.927
3813	0.01157	aquaporin 7 (AQP7), mRNA /cds=(173,1201) /gb=NM_001170 /gi=4502186 /ug=Hs.25475 /len=1258	NM_001170	Hs.25475
5985	0.01157	interleukin 6 signal transducer (gp130, oncostatin M receptor) (IL6ST), mRNA /cds=(256,3012) /gb=NM_002184 /gi=4504674 /ug=Hs.82065 /len=3085	NM_002184	Hs.82065
7463	0.01157	early growth response 1 (EGR1), mRNA /cds=(271,1902) /gb=NM_001964 /gi=4503492 /ug=Hs.326035 /len=3132	NM_001964	Hs.326035
7496	0.01157	Novel mRNA from chromosome 1, which has similarities to BAT2 genes /cds=(58,8163) /gb=AL096857 /gi=5541862 /ug=Hs.69559 /len=10174	AL096857	Hs.69559
14452	0.01157	no match		
6674	0.01157	serine/threonine-protein kinase PRP4 (PRP4), mRNA /cds=(65,3088) /gb=NM_003913 /gi=17999534 /ug=Hs.198891 /len=3202	NM_003913	Hs.198891
6344	0.010844	malic enzyme 1, NADP()-dependent, cytosolic (ME1), mRNA /cds=(108,1826) /gb=NM_002395 /gi=13435400 /ug=Hs.14732 /len=2212	NM_002395	Hs.14732
6809	0.010844	eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864	NM_001967	Hs.173912
8702	0.010844	sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA /cds=(106,1440) /gb=NM_152594 /gi=22749220 /ug=Hs.302718 /len=3816	NM_152594	Hs.302718
11582	0.010844	RC1-NN0073-090500-012-f02 NN0073 cDNA, mRNA sequence /gb=AW898615 /gi=8062820 /ug=Hs.130729 /len=660	AW898615	Hs.130729

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
6331	0.010844	decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(66,1211) /gb=NM_000574 /gi=10835142 /ug=Hs.1369 /len=2102	NM_000574	Hs.1369
4784	0.010159	clone IMAGE:5312122, mRNA /gb=BC039457 /gi=24659919 /ug=Hs.107479 /len=1630	BC039457	Hs.107479
14022	0.010159	cDNA: FLJ20973 fis, clone ADSU01580, highly similar to HS222E13A Isoform 1 of a novel mRNA from chromosome 22. /gb=AK024626 /gi=10436944 /ug=Hs.334836 /len=3387	AK024626	Hs.334836
8602	0.010159	clone IMAGE:5217034, mRNA /gb=BC041468 /gi=27370762 /ug=Hs.434746 /len=1884	BC041468	Hs.434746
5512	0.010159	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328
11535	0.010159	spindlin 1 mRNA, complete cds	AF317228	Hs.289043
9632	0.009511	clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651	BC013590	Hs.2437
10036	0.009511	src 3 domain-containing protein HIP-55 (HIP-55), mRNA /cds=(31,1326) /gb=NM_014063 /gi=21361669 /ug=Hs.183373 /len=2170	NM_014063	Hs.183373
8365	0.009511	hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(175,735) /gb=NM_018184 /gi=8922600 /ug=Hs.104222 /len=2944	NM_018184	Hs.104222
10073	0.008899	chemokine (C-C motif) receptor 1 (CCR1), mRNA /cds=(63,1130) /gb=NM_001295 /gi=4502630 /ug=Hs.301921 /len=2156	NM_001295	Hs.301921
4163	0.008899	coactivator for steroid receptors (COASTER), mRNA /cds=(226,3267) /gb=NM_015555 /gi=20127147 /ug=Hs.172329 /len=4999	NM_015555	Hs.172329
8942	0.008322	mRNA for Sec24 protein (Sec24A isoform), partial /cds=(1,3237) /gb=AJ131244 /gi=3947687 /ug=Hs.211612 /len=5967	AJ131244	Hs.211612
7679	0.008322	cAMP responsive element binding protein 1 (CREB1), transcript variant B, mRNA /cds=(182,1207) /gb=NM_134442 /gi=22219460 /ug=Hs.79194 /len=3006	NM_134442	Hs.79194
6704	0.008322	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570
10198	0.008322	ze65h12.s1 Soares retina N2b4HR cDNA clone IMAGE:363911 3', mRNA sequence /clone=IMAGE:363911 /clone_end=3' /gb=AA021186 /gi=1484920 /ug=Hs.226306 /len=422	AA021186	Hs.226306
3958	0.008322	CGI-150 protein (CGI-150), mRNA /cds=(202,1716) /gb=NM_016080 /gi=7705645 /ug=Hs.279061 /len=2580	NM_016080	Hs.279061

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
2961	0.007778	DNA sequence from clone RP11-258C19 on chromosome Xp11.21-11.23, complete sequence	AL139396	
11579	0.007516	BX096653 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGp998I121022, mRNA sequence /clone=IMAGp998I121022;_IMAGE:434771 /gb=BX096653 /gi=27842914 /ug=Hs.114074 /len=782	BX096653	Hs.114074
4269	0.007265	D-dopachrome tautomerase (=U49785; Y11151)	AF058293	
14699	0.007265	similar to protein that is immuno-reactive with anti-PTH polyclonal antibodies (LOC286623), mRNA	XM_210342	
822	0.007265	FAT tumor suppressor 1 (Drosophila) (FAT), mRNA /cds=(187,13959) /gb=NM_005245 /gi=4885228 /ug=Hs.166994 /len=14756	NM_005245	Hs.166994
9441	0.006782	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA /cds=(767,1375) /gb=NM_023012 /gi=20127619 /ug=Hs.81648 /len=1878	NM_023012	Hs.81648
5267	0.006327	RNA binding motif protein 6 (RBM6), mRNA /cds=(134,3505) /gb=NM_005777 /gi=5032032 /ug=Hs.173993 /len=3639	NM_005777	Hs.173993
5911	0.005899	mitochondrion, complete genome	NC_001807	
5030	0.005119	clone IMAGE:3630431, mRNA /gb=BC017319 /gi=16878242 /ug=Hs.28631 /len=3540	BC017319	Hs.28631
733	0.005119	squamous cell carcinoma antigen recognised by T cells 3 (SART3), mRNA /cds=(8,2899) /gb=NM_014706 /gi=21327689 /ug=Hs.116875 /len=3776	NM_014706	Hs.116875
4286	0.005119	aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 1, mRNA	NM_001135	Hs.2159
12678	0.004764	BAC clone RP11-343F11 from 2, complete sequence	AC064860	
2963	0.004764	cDNA FLJ40109 fis, clone TESTI2007685. /gb=AK097428 /gi=21757181 /ug=Hs.377146 /len=2007	AK097428	Hs.377146
6787	0.004764	hypothetical protein FLJ21827 (FLJ21827), mRNA /cds=(379,1446) /gb=NM_020153 /gi=21361819 /ug=Hs.334360 /len=1834	NM_020153	Hs.334360
13707	0.004431	lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), mRNA /cds=(41,1240) /gb=NM_000235 /gi=4557720 /ug=Hs.85226 /len=2493	NM_000235	Hs.85226
10906	0.004431	cDNA FLJ39740 fis, clone SMINT2016477. /gb=AK097059 /gi=21756705 /ug=Hs.432907 /len=1987	AK097059	Hs.432907
12778	0.004431	cDNA FLJ33834 fis, clone CTONG2004264, moderately similar to NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK. /cds=(6,2381) /gb=AK091153 /gi=21749455 /ug=Hs.378738 /len=2712	AK091153	Hs.378738

Table 3V Genes Corresponding to Steroids Only 362

Spot	p-value	Description	Accession	Unigene
3929	0.004118	similar to KIAA0187 gene product, clone IMAGE:4122983, mRNA /gb=BC033148 /gi=21620041 /ug=Hs.380041 /len=1936	BC033148	Hs.380041
6797	0.004118	cDNA FLJ11469 fis, clone HEMBA1001658. /gb=AK021531 /gi=10432731 /ug=Hs.224398 /len=1665	AK021531	Hs.224398
13152	0.004118	cDNA FLJ13545 fis, clone PLACE1006867. /gb=AK023607 /gi=10435587 /ug=Hs.421529 /len=1887	AK023607	Hs.421529
4190	0.004118	protein x 0001 (LOC51185), mRNA /cds=(34,1044) /gb=NM_016302 /gi=10047097 /ug=Hs.18925 /len=1668	NM_016302	Hs.18925
10341	0.004118	chromosome 14 DNA sequence BAC R-248B10 of library RPCI-11 from chromosome 14 of complete sequence	AL163853	
7680	0.003825	tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA /cds=(77,910) /gb=NM_007115 /gi=26051242 /ug=Hs.29352 /len=1440	NM_007115	Hs.29352
9635	0.003055	hypothetical protein FLJ11838 (FLJ11838), mRNA /cds=(8,862) /gb=NM_024664 /gi=13375918 /ug=Hs.72531 /len=1430	NM_024664	Hs.72531
5328	0.00283	CDC20 cell division cycle 20 (S. cerevisiae) (CDC20), mRNA /cds=(111,1610) /gb=NM_001255 /gi=4557436 /ug=Hs.82906 /len=1686	NM_001255	Hs.82906
642	0.00283	centrin, EF-hand protein, 2 (CETN2), mRNA /cds=(48,566) /gb=NM_004344 /gi=4757901 /ug=Hs.82794 /len=1087	NM_004344	Hs.82794
10438	0.002072	we90c07.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2348364 3', mRNA sequence /clone=IMAGE:2348364 /clone_end=3' /gb=AI797677 /gi=5363149 /ug=Hs.199882 /len=554	AI797677	Hs.199882
11630	0.001913	uncharacterized hypothalamus protein HT007 (HT007), mRNA /cds=(228,887) /gb=NM_018480 /gi=8923801 /ug=Hs.24371 /len=1172	NM_018480	Hs.24371
14237	4.86E-04	df13e04.y1 Morton Fetal Cochlea cDNA clone IMAGE:2483406 5', mRNA sequence /clone=IMAGE:2483406 /clone_end=5' /gb=AW020719 /gi=5874249 /ug=Hs.233140 /len=357	AW020719	Hs.233140
8618	1.12E-04	EST(HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA)	BG896206.1	